

<!--StartFragment-->RESULT 5

AAM49641

ID AAM49641 standard; protein; 836 AA.

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AC AAM49641;

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DT 17-MAY-2002 (first entry)

XX

DE Human tumour-associated antigen B345 protein SEQ ID NO 4.

XX

KW Tumour-associated antigen; human; B345; cytostatic; cell communication; cell interaction; signal transduction; metastasis; cancer; colon; immunotherapy; carcinoma; lung; diagnosis.

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OS Homo sapiens.

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PN WO200204508-A1.

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PD 17-JAN-2002.

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PF 05-JUL-2001; 2001WO-EP007705.

XX

PR 07-JUL-2000; 2000DE-01033080.

PR 19-APR-2001; 2001DE-01019294.

XX

PA (BOEHRINGER) BOEHRINGER INGELHEIM INT GMBH.

XX

PI Schweifer N, Scherl-Mostageer M, Sommergruber W, Abseher R;

XX

DR WPI; 2002-171704/22.

DR N-PSDB; ABA99507.

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PT New tumor-associated antigen B345, useful for diagnosis and immunotherapy of tumors, also related nucleic acid and antibodies.

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PS Claim 1; Page 85-88; 102pp; German.

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CC This invention describes a novel tumour-associated antigen, designated B345 which has cytostatic activity. B345 is involved in communication, interaction and/or signal transduction with extracellular components and ligands, especially in the metastatic potential of cancers, particularly of the colon. B345 or its immunogenic fragments, also the DNA that encodes it, are useful for immunotherapy of cancer, particularly carcinoma of lung or colon. Antibodies raised against B345 are useful for treatment and diagnosis of cancers that are associated with B345 expression, including their use for targeted delivery of cytotoxic or radioactive agents. Probes derived from B345 can be used to detect tumour-specific mutations in the B345 sequence, and can be used to screen for B345 specific modulators. This sequence represents a human B345 tumour-associated antigen described in the invention

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SQ Sequence 836 AA;

Query Match 99.8%; Score 4385; DB 5; Length 836;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 834; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGLNCGVSIALLGVLRLGAAARLPRGAEAEFEIALPRESNITVLIKLGPTLAKPCYIVI 60
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Db 1 MAGLNCGVSIALLGVLRLGAAARLPRGAEAEFEIALPRESNITVLIKLGPTLAKPCYIVI 60

Qy 61 SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSPCPFGEVQLQPSTSLLPT 120
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Db 61 SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSPCPFGEVQLQPSTSLLPT 120

Qy 121 LNRTF1IWVDKAHKSIGLELQFSPRQLRQ1GPGESCPDGVTHS1SISGRIDATVVRIGTFCSN 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 LNRTF1IWVDKAHKSIGLELQFSPRQLRQ1GPGESCPDGVTHS1SISGRIDATVVRIGTFCSN 180

Qy 181 GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 181 GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY 240

Qy 241 PEGFPEDELMTWQFVVPAHLRASVSLNFNLNSNCERKEERVEYYIPGSTTNPEVFKLEDK 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 241 PEGFPEDELMTWQFVVPAHLRASVSLNFNLNSNCERKEERVEYYIPGSTTNPEVFKLEDK 300

Qy 301 QPGNMAGNFNLSQLQGCDQDAQSPGILRQLQFQVLVQHPQNESNK1YVVDLSNERAMSLTIE 360
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Db 301 QPGNMAGNFNLSQLQGCDQDAQSPGILRQLQFQVLVQHPQNESNK1YVVDLSNERAMSLTIE 360

Qy 361 PRPVKQSRKFVPGCFVCLERSCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH 420
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Db 361 PRPVKQSRKFVPGCFVCLERSCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH 420

Qy 421 RYCQRKSYSLSQVPSDILHLPVLEHDFSWKLVPKDRSLSLVLPVPAQKLQOHTHEKPCNTSF 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||

Db 421 RYCQRKSYSLSQVPSDILHLPVLEHDFSWKLVPKDRSLSLVLPVPAQKLQOHTHEKPCNTSF 480

Qy 481 SYLVAISAIPSQDLYFGSFCPGGSIKQIQVKQNIISVTLRTFAPSFRQEASRQGLTVSFIPY 540
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Db 481 SYLVAISAIPSQDLYFGSFCPGGSIKQIQVKQNIISVTLRTFAPSFRQEASRQGLTVSFIPY 540

Qy 541 FKEEGVFTVTPDTSKVYLRTPNWDRGLPSLTSVSNWISVPRDQVACLTFFKERGVVCQ 600
 ||||||||||||||||||||||||||||||||||||||||||||||

Db 541 FKEEGVFTVTPDTSKVYLRTPNWDRGLPSLTSVSNWISVPRDQVACLTFFKERGVVCQ 600

Qy 601 TGRAFMIIQEQRTRAAEIFSLDEDVLPKPSFHHSFHWVNISNCSPSGKQLDLLFSTVLT 660
 ||||||||||||||||||||||||||||||||||||||||||||||

Db 601 TGRAFMIIQEQRTRAAEIFSLDEDVLPKPSFHHSFHWVNISNCSPSGKQLDLLFSTVLT 660

Qy 661 PRTVDLTVILIAVGGGVLLSALGGLIICCVKKKKKTNKGPAVG1YNGNINTEMPRQPK 720
 ||||||||||||||||||||||||||||||||||||||||||||||

Db 661 PRTVDLTVILIAVGGGVLLSALGGLIICCVKKKKKTNKGPAVG1YNGNINTEMPRQPK 720

Qy 721 KFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGFLQPEVDTYRPFQGTMGVCPSPPTIC 780
 ||||||||||||||||||||||||||||||||||||||||||||||

Db 721 KFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGFLQPEVDTYRPFQGTMGVCPSPPTIC 780

Qy 781 SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKTDIPLLSTQEPMEPAE 836
 ||||||||||||||||||||||||||||||||||||||||||||||

Db 781 SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKTDIPLLNTQEPMEPAE 836

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